



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/506,455

DATE: 09/09/2004  
TIME: 16:17:57

Input Set : A:\X-15648.ST25.txt  
Output Set: N:\CRF4\09092004\J506455.raw

3 <110> APPLICANT: Beals, John  
4 Kuchibhotla, Uma  
6 <120> TITLE OF INVENTION: HETEROLOGOUS G-CSF FUSION PROTEINS  
8 <130> FILE REFERENCE: X-15648  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/506,455  
C--> 10 <141> CURRENT FILING DATE: 2004-08-31  
10 <150> PRIOR APPLICATION NUMBER: PCT/US03/03120  
11 <151> PRIOR FILING DATE: 2003-02-21  
13 <160> NUMBER OF SEQ ID NOS: 66  
15 <170> SOFTWARE: PatentIn version 3.2  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 174  
19 <212> TYPE: PRT  
20 <213> ORGANISM: Artificial Sequence  
22 <220> FEATURE:  
23 <223> OTHER INFORMATION: synthetic construct  
26 <220> FEATURE:  
27 <221> NAME/KEY: MISC\_FEATURE  
28 <222> LOCATION: (17)..(17)  
29 <223> OTHER INFORMATION: Xaa at position 17 is Cys, Ala, Leu, Ser, or Glu;  
31 <220> FEATURE:  
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33 <222> LOCATION: (37)..(37)  
34 <223> OTHER INFORMATION: Xaa at position 37 is Ala or Asn;  
36 <220> FEATURE:  
37 <221> NAME/KEY: MISC\_FEATURE  
38 <222> LOCATION: (38)..(38)  
39 <223> OTHER INFORMATION: Xaa at position 38 is Thr, or any other amino acid except Pro;  
41 <220> FEATURE:  
42 <221> NAME/KEY: MISC\_FEATURE  
43 <222> LOCATION: (39)..(39)  
44 <223> OTHER INFORMATION: Xaa at position 39 is Tyr, Thr, or Ser;  
46 <220> FEATURE:  
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48 <222> LOCATION: (57)..(57)  
49 <223> OTHER INFORMATION: Xaa at position 57 is Pro or Val;  
51 <220> FEATURE:  
52 <221> NAME/KEY: MISC\_FEATURE  
53 <222> LOCATION: (58)..(58)  
54 <223> OTHER INFORMATION: Xaa at position 58 is Trp or Asn;  
56 <220> FEATURE:  
57 <221> NAME/KEY: MISC\_FEATURE  
58 <222> LOCATION: (59)..(59)

ENTERED

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59 <223> OTHER INFORMATION: Xaa at position 59 is Ala or any other amino acid except Pro;  
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64 <223> OTHER INFORMATION: Xaa at position 60 is Pro, Thr, Asn, or Ser;  
66 <220> FEATURE:  
67 <221> NAME/KEY: MISC\_FEATURE  
68 <222> LOCATION: (61)..(61)  
69 <223> OTHER INFORMATION: Xaa at position 61 is Leu, or any other amino acid except  
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72 <221> NAME/KEY: MISC\_FEATURE  
73 <222> LOCATION: (62)..(62)  
74 <223> OTHER INFORMATION: Xaa at position 62 is Ser or Thr;  
76 <220> FEATURE:  
77 <221> NAME/KEY: MISC\_FEATURE  
78 <222> LOCATION: (63)..(63)  
79 <223> OTHER INFORMATION: Xaa at position 63 Ser or Asn;  
81 <220> FEATURE:  
82 <221> NAME/KEY: MISC\_FEATURE  
83 <222> LOCATION: (64)..(64)  
84 <223> OTHER INFORMATION: Xaa at position 64 is Cys or any other amino acid except Pro;  
86 <220> FEATURE:  
87 <221> NAME/KEY: MISC\_FEATURE  
88 <222> LOCATION: (65)..(65)  
89 <223> OTHER INFORMATION: Xaa at position 65 is Pro, Ser, or Thr;  
91 <220> FEATURE:  
92 <221> NAME/KEY: MISC\_FEATURE  
93 <222> LOCATION: (66)..(66)  
94 <223> OTHER INFORMATION: Xaa at position 66 is Ser or Thr;  
96 <220> FEATURE:  
97 <221> NAME/KEY: MISC\_FEATURE  
98 <222> LOCATION: (67)..(67)  
99 <223> OTHER INFORMATION: Xaa at position 67 is Gln or Asn;  
101 <220> FEATURE:  
102 <221> NAME/KEY: MISC\_FEATURE  
103 <222> LOCATION: (68)..(68)  
104 <223> OTHER INFORMATION: Xaa at position 68 is Ala or any other amino acid except  
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107 <221> NAME/KEY: MISC\_FEATURE  
108 <222> LOCATION: (69)..(69)  
109 <223> OTHER INFORMATION: Xaa at position 69 is Leu, Thr, or Ser;  
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113 <222> LOCATION: (93)..(93)  
114 <223> OTHER INFORMATION: Xaa at position 93 is Glu or Asn;  
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117 <221> NAME/KEY: MISC\_FEATURE  
118 <222> LOCATION: (94)..(94)  
119 <223> OTHER INFORMATION: Xaa at position 94 is Gly or any other amino acid except  
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 123 <222> LOCATION: (95)..(95)  
 124 <223> OTHER INFORMATION: Xaa at position 95 is Ile, Asn, Ser, or Thr;  
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 128 <222> LOCATION: (97)..(97)  
 129 <223> OTHER INFORMATION: Xaa at position 97 is Pro, Ser, Thr, or Asn;  
 131 <220> FEATURE:  
 132 <221> NAME/KEY: MISC\_FEATURE  
 133 <222> LOCATION: (133)..(133)  
 134 <223> OTHER INFORMATION: Xaa at position 133 is Thr or Asn;  
 136 <220> FEATURE:  
 137 <221> NAME/KEY: MISC\_FEATURE  
 138 <222> LOCATION: (134)..(134)  
 139 <223> OTHER INFORMATION: Xaa at position 134 is Gln or any other amino acid except  
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 142 <221> NAME/KEY: MISC\_FEATURE  
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 148 <222> LOCATION: (141)..(141)  
 149 <223> OTHER INFORMATION: Xaa at position 141 is Ala or Asn;  
 151 <220> FEATURE:  
 152 <221> NAME/KEY: MISC\_FEATURE  
 153 <222> LOCATION: (142)..(142)  
 154 <223> OTHER INFORMATION: Xaa at position 142 is Ser or any other amino acid except  
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 158 <222> LOCATION: (143)..(143)  
 159 <223> OTHER INFORMATION: Xaa at position 143 is Ala, Ser, or Thr.  
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 164 1 5 10 15  
 W--> 167 Xaa Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln  
 168 20 25 30  
 171 Glu Lys Leu Cys Xaa Xaa Xaa Lys Leu Cys His Pro Glu Glu Leu Val  
 172 35 40 45  
 175 Leu Leu Gly His Ser Leu Gly Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 176 50 55 60  
 179 Xaa Xaa Xaa Xaa Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
 180 65 70 75 80  
 183 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Xaa Xaa Xaa Ser  
 184 85 90 95  
 187 Xaa Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
 188 100 105 110  
 191 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
 192 115 120 125

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195 Ala Leu Gln Pro Xaa Xaa Xaa Ala Met Pro Ala Phe Xaa Xaa Xaa Phe  
 196 130 135 140  
 199 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe  
 200 145 150 155 160  
 203 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
 204 165 170  
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 209 <212> TYPE: DNA  
 210 <213> ORGANISM: Artificial Sequence  
 212 <220> FEATURE:  
 213 <223> OTHER INFORMATION: synthetic construct  
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 218 ggacggtcga gggacggggt ctgcgaaggac gagttcgct tagagcaagt gaggaaagatc 120  
 220 caggcgatg ggcgcagcgct ccagcggaat ctcgttcaact ccttctaggt cccgctaccg 180  
 222 cgtcgcgagg tcgagaagct gtgtgccacc tacaagctgt gcccacccgaa ggagctggtg 240  
 224 ctcttcgaca cacgggtggat gttcgacacg gtggggctcc tcgaccacct gctcggacac 300  
 226 tctctggca tcccctggc tcccctgagc agctgcgacg agcctgtgac agacccgttag 360  
 228 gggacccgag gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc 420  
 230 caactccata gcgggtcggt ccgggacgtc gaccgtccga cgaactcggt tgaggtatcg 480  
 232 ggcctttcc tctaccaggc gtcctgtcag gcccctggaa ggatctcccc ggaaaaggag 540  
 234 atggtccccg aggacgtccg ggaccttccc tagaggccc agttgggtcc caccctggac 600  
 236 acactgcagc tggacgtcgcc gacggggctc aaccctgggt ggaacctgtg tgacgtcgac 660  
 238 ctgcagcggc tgtttgcac caccatctgg cagcagatgg aagaactggg aatggccct 720  
 240 aaacgggtggt ggttagaccgt cgtctacccctt gtcggccctt accggggagc cctgcagccc 780  
 242 aaccagaccg ccatgcggc cttcgcctt gtttccggg acgtcggtt ggtctggcg 840  
 244 tacggccgga agcggagacg aaagcagcgc cgggcaggag ggttcctgt tgctcccat 900  
 246 ctgcagagct tcgtcgccgc cctgcctccc caggaccaac ggagggtaga cgtctcgaa 960  
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 266 caggcgatg ggcgcagcgct ccagcggaat ctcgttcaact ccttctaggt cccgctaccg 180  
 268 cgtcgcgagg tcgagaagct gtgtgccacc tacaagctgt gcccacccgaa ggagctggtg 240  
 270 ctcttcgaca cacgggtggat gttcgacacg gtggggctcc tcgaccacct gctcggacac 300  
 272 tctctggca tcccctggc tcccctgagc agctgcgacg agcctgtgac agacccgttag 360  
 274 gggacccgag gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc 420  
 276 caactccata gcgggtcggt ccgggacgtc gaccgtccga cgaactcggt tgaggtatcg 480  
 278 ggcctttcc tctaccaggc gtcctgtcag gcccctggaa ggatctcccc ggaaaaggag 540  
 280 atggtccccg aggacgtccg ggaccttccc tagaggccc agttgggtcc caccctggac 600  
 282 acactgcagc tggacgtcgcc gacggggctc aaccctgggt ggaacctgtg tgacgtcgac 660

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284	ctgcagcggc	tgttgcac	caccatctgg	cagcagatgg	aagaactggg	aatggccct	720
286	aaacgggtgt	ggtagaccgt	cgtctacott	cttgcacccct	accggggagc	cctgcagccc	780
288	acccagggtg	ccatgcggc	cttcaactct	accttccggg	acgtcgggtg	ggtcccacgg	840
290	tacggccgga	agttgagatg	gaagcagcgc	cgggcaggag	gggtccttgt	tgcctccat	900
292	ctgcagagct	tcgtcgcggc	ccgtcctccc	caggaccaac	ggagggtaga	cgtctcgaag	960
294	ctggaggtgt	cgtaccgcgt	cttaaggcac	cttgcacccagc	ccgacctcca	cagcatggcg	1020
296	cagaattccg	tggaacgggt	cggg				1044
299	<210>	SEQ ID NO:	4				
300	<211>	LENGTH:	1044				
301	<212>	TYPE:	DNA				
302	<213>	ORGANISM:	Artificial Sequence				
304	<220>	FEATURE:					
305	<223>	OTHER INFORMATION:	synthetic construct				
307	<400>	SEQUENCE:	4				
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310	ggacggtcga	gggacgggt	ctcgaaggac	gagtgcct	tagagcaagt	gaggaagatc	120
312	cagggcgatg	gcgcagcgct	ccagcggaa	ctcggtca	ccttctaggt	cccgctaccg	180
314	cgtcgcgagg	tcgagaagct	gtgtaa	accaggctgt	gccaccccg	ggagctggtg	240
316	ctcttcgaca	cattgtgg	gttcgacacg	gtggggctcc	tcgaccac	gctcgac	300
318	tctctggca	tcccctggc	tcccctgagc	agctgcgac	agcctgtgac	agacccgtag	360
320	gggacccgag	gggactcg	gacgccc	caggccctgc	agctggcagg	ctgcttgagc	420
322	caactccata	gcgggtcggt	ccgggacgtc	gaccgtccg	cgaactcggt	tgaggtatcg	480
324	ggcctttcc	tctaccagg	gtccctgcag	gccctggaag	ggatctccc	ggaaaaggag	540
326	atggtccccg	aggacgtcc	ggac	tagaggccc	agttgggtcc	caccttggac	600
328	acactgcagc	tggacgtc	cgacgggc	aaccagggt	ggaacctgt	tgacgtcgac	660
330	ctgcagcggc	tgttgcac	caccatctgg	cagcagatgg	aagaactggg	aatggccct	720
332	aaacgggtgt	ggtagaccgt	cgtctacott	cttgcaccc	accggggagc	cctgcagccc	780
334	acccagggtg	ccatgcggc	cttcgcct	gtttccggg	acgtcgggtg	ggtcccacgg	840
336	tacggccgga	agcggagacg	aaagcagcgc	cgggcaggag	gggtccttgt	tgcctccat	900
338	ctgcagagct	tcgtcgcggc	ccgtcctccc	caggaccaac	ggagggtaga	cgtctcgaag	960
340	ctggaggtgt	cgtaccgcgt	cttaaggcac	cttgcacccagc	ccgacctcca	cagcatggcg	1020
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348	<213>	ORGANISM:	Artificial Sequence				
350	<220>	FEATURE:					
351	<223>	OTHER INFORMATION:	synthetic construct				
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356	ggacggtcga	gggacgggt	ctcgaaggac	gagtgcct	tagagcaagt	gaggaagatc	120
358	cagggcgatg	gcgcagcgct	ccagcggaa	ctcggtca	ccttctaggt	cccgctaccg	180
360	cgtcgcgagg	tcgagaagct	gtgtgccacc	tacaaggctgt	gccaccccg	ggagctggtg	240
362	ctcttcgaca	cacgggtggat	gttcgacacg	gtggggctcc	tcgaccac	gctcgac	300
364	tctctggca	tcccctggc	taacactagc	agctgcgac	agcctgtgac	agacccgtag	360
366	gggacccgat	tggactcctc	gacgccc	caggccctgc	agctggcagg	ctgcttgagc	420
368	caactccata	gcgggtcggt	ccgggacgtc	gaccgtccg	cgaactcggt	tgaggtatcg	480
370	ggcctttcc	tctaccagg	gtccctgcag	gccctggaag	ggatctccc	ggaaaaggag	540
372	atggtccccg	aggacgtcc	ggac	tagaggccc	agttgggtcc	caccttggac	600

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 17, 37, 38, 39, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 93, 94  
Seq#:1; Xaa Pos. 95, 97, 133, 134, 135, 141, 142, 143

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16  
M:341 Repeated in SeqNo=1